GenCore version 4.5

SM nucleic - nucleic search, using sw model

Run on: November 19, 2001, 16:43:24 ; Search time 1187.52 Seconds
(without alignments)
4991.023 Million cell updates/sec

Title: US-09-516-052-1
Perfect score: 627
Sequence: 1 atgaccaactcaqtcatact.....attatqqtcaqtataaatqa 627

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000300

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: qb_est1:*
2: qb_est2:*
3: qb_est3:*
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7: qb_est7:*
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254: em_qss_rod7:*
255: em_qss_rod8:*
256: qb_qss45:*
257: qb_qss46:*
258: qb_qss47:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	420.4	51.1	765	226	AQ251011	AQ251011 T28A5-Sp6
2	419.2	50.4	459	41	AV566418	AV566418 AV566418
3	266.4	42.5	438	41	AV558190	AV558190 AV558190
4	209	33.3	479	41	AV561940	AV561940 AV561940
5	182.4	29.1	497	155	BG551755	BG551755 sad42f11.y
6	182.4	29.1	551	116	AW432980	AW432980 si03a01.y
7	182.4	29.1	594	120	AW756413	AW756413 si21a12.y
8	180.2	28.7	476	151	BF595304	BF595304 su76104.y
9	165.6	26.4	645	107	AG088581	AG088581 AG088581
10	160	25.5	528	147	BE603222	BE603222 HV3MEB010
11	159.2	25.4	488	119	AW719547	AW719547 LjNEST6a3
12	159.2	25.4	561	119	AW720671	AW720671 LjNEST6a3
13	158	25.2	441	147	AL509098	AL509098 AL509098
14	157.2	25.1	594	105	AL506199	AL506199 AL506199
15	150.8	24.1	535	120	AW754604	AW754604 PC04B12.P
16	140.8	22.5	887	144	BE065056	BE065056 HV_CEb002
17	140.2	22.4	418	40	AV424305	AV424305 AV424305
18	139.4	22.2	526	123	AW981720	AW981720 PC15H07.P
19	138.6	22.1	924	167	BE418716	BE418716 SCL074.B0
20	137.8	21.9	328	118	AW585586	AW585586 EST417609
21	137.6	21.9	476	146	BE496857	BE496857 WHE0761_D
22	136.8	21.8	561	41	AV550943	AV550943 AV550943
23	136.2	21.7	595	146	BE263449	BE263449 HV_CEa000
24	136.2	21.7	595	146	BE263455	BE263455 HV_CEa003
25	136	21.7	685	175	BG263362	BG263362 WHE2341_B
26	141.2	21.4	575	104	AI995140	AI995140 701502287
27	132.8	21.2	431	168	BF715909	BF715909 saa11e08.
28	131	20.9	464	158	H76589	H76589 19294 Lambd
29	130.8	20.9	422	120	AW760103	AW760103 si58b03.y
30	126.6	20.2	638	152	BG314203	BG314203 WHP2460_F
31	128	20.4	364	162	BE060015	BE060015 sn39h06.y
32	127	20.3	593	136	BE516510	BE516510 WHE611_D1
33	127	20.3	702	150	BF585526	BF585526 FM1_23_E0
34	127	20.3	720	167	BE413647	BE413647 SCU001.E1
35	126.6	20.2	512	120	AW775623	AW775623 EST434688
36	126.6	20.2	661	151	BF651151	BF651151 NF101B10E
37	126.6	20.2	682	123	AW980494	AW980494 EST391647
38	126.2	20.1	465	116	AW459387	AW459387 sh23f03.y
39	126	20.1	616	151	BF597252	BF597252 su96c06.y
40	125	19.9	548	40	AV437366	AV437366 AV437366
41	125	19.9	540	40	AV432410	AV432410 AV432410
42	124.8	19.9	524	40	AV434349	AV434349 AV434349
43	124.8	19.9	528	162	BE021041	BE021041 sa64d05.y
44	124.4	19.8	633	103	AI900024	AI900024 sb97q11.y
45	123.4	19.7	454	164	BE210041	BE210041 so38b01.y

ALIGNMENTS

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RESULT  1
AQ251011
LOCUS       AQ251011        765 bp    DNA             GSS       07-OCT-1998
DEFINITION  T28A5 SP6 IAMU Arabidopsis thaliana genomic clone T28A5, DNA
            sequence.
ACCESSION   AQ251011
VERSION     AQ251011.1  GI:3704077
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 765)
  AUTHORS   Fu,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Chiba,F., Jun,H. and
            Ecker,J.
  TITLE     BAC End Sequences at AIGC
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Ecker J.
            Arabidopsis Thaliana Genome Center
            University of Pennsylvania
            Dept. of Biology, University of Pennsylvania, Philadelphia, PA
            19104
            Tel: 215-898-9384
            Fax: 215-898-8780
            Email: jecker@atgenome.bio.upenn.edu
            Seq primer: Sp6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1..765
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia"
                     /db_xref="taxon:3702"
                     /clone="T28A5"
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                     /sex="hermaphrodite"
                     /note "Vector: BeloBAC11; Site_1: HindIII; Site_2: HindIII
                     ; Produced by Rod Wing"
BASE COUNT      206 a    138 c    161 g    254 t      6 others
ORIGIN
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Query Match 51.1%; Score 420.4; DB 226; Length 765;
Best Local Similarity 98.2%; Pred. No. 4.5e-92;
Matches 324; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy      298 cttgggttcgataaatacgtcgaaccccctcaccgtgttcattaacccgtcacccgtgaggata 357
            ||||||| |  ||||||||||||||||||||||||||||||||||||| |||| ||||||||||
Db       66 CTTGGGTACTTTAACTACGTGGACCCCCTCACCGTGTTCATTAGCCGGCCCCGTGAGATA 125

Qy      358 gagaccgatcgtgattctgtcacttagaggtgagccacccgtcgttgagacaaacctatgga 417
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      126 GAGACCGATCGTGGTTCTGCACTTAGAGGTGAGCCACCGTCGTTGAGACAAACCTATGGA 185

Qy      418 qqaaatqqtattqqqtttcacqqcccatctcatqqcctacctcctccqqqtccttatqqt 477
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      186 GGAAATGGTATTGGGTTTCACGGCCCATCTCATGGCCTACCTCCTCCGGGTCCTTATGGT 245

Qy      478 tatqqtatqttqqaccaatccatqattatqqoaqqtqqtccqtactaccaaaacqqqtcq 537
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      246 TATGGTATGTTGGACCAATCCATGGTTATGGGAGGTGGTCGGTACTACCAAAACGGGTCG 305

Qy      538 tcqqqtccaatatqaatccagtgttcatqatqcctttcqttcttcattaacqqaatqccq 597
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      306 TCGGGTCAAGATGAATCCAGTGTTGGTGGTGGCTCTTCGTCTTCCATTAACGGAATGCCG 365

Qy      598 qctttqaccattatqqtcaqtataaqtqa 627
            |||||||||||||||||||||||||||||
Db      366 GCTTTGACCATTATGGTCAGTATAAGTGA 395
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RESULT  2
AV566418/C
LOCUS       AV566418        459 bp    mRNA            EST       07-SEP-2000
DEFINITION  AV566418 Arabidopsis thaliana green siliques Columbia Arabidopsis
            thaliana cDNA clone SQ21A11F 3', mRNA sequence.
ACCESSION   AV566418
VERSION     AV566418.1  GI:8737870
KEYWORDS    EST.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
  TITLE     A large scale analysis of cDNA in Arabidopsis thaliana: Generation
            of 12,028 non-redundant expressed sequence tags from normalized and
            size-selected cDNA libraries
  JOURNAL   DNA Res. 7, 175-180 (2000)
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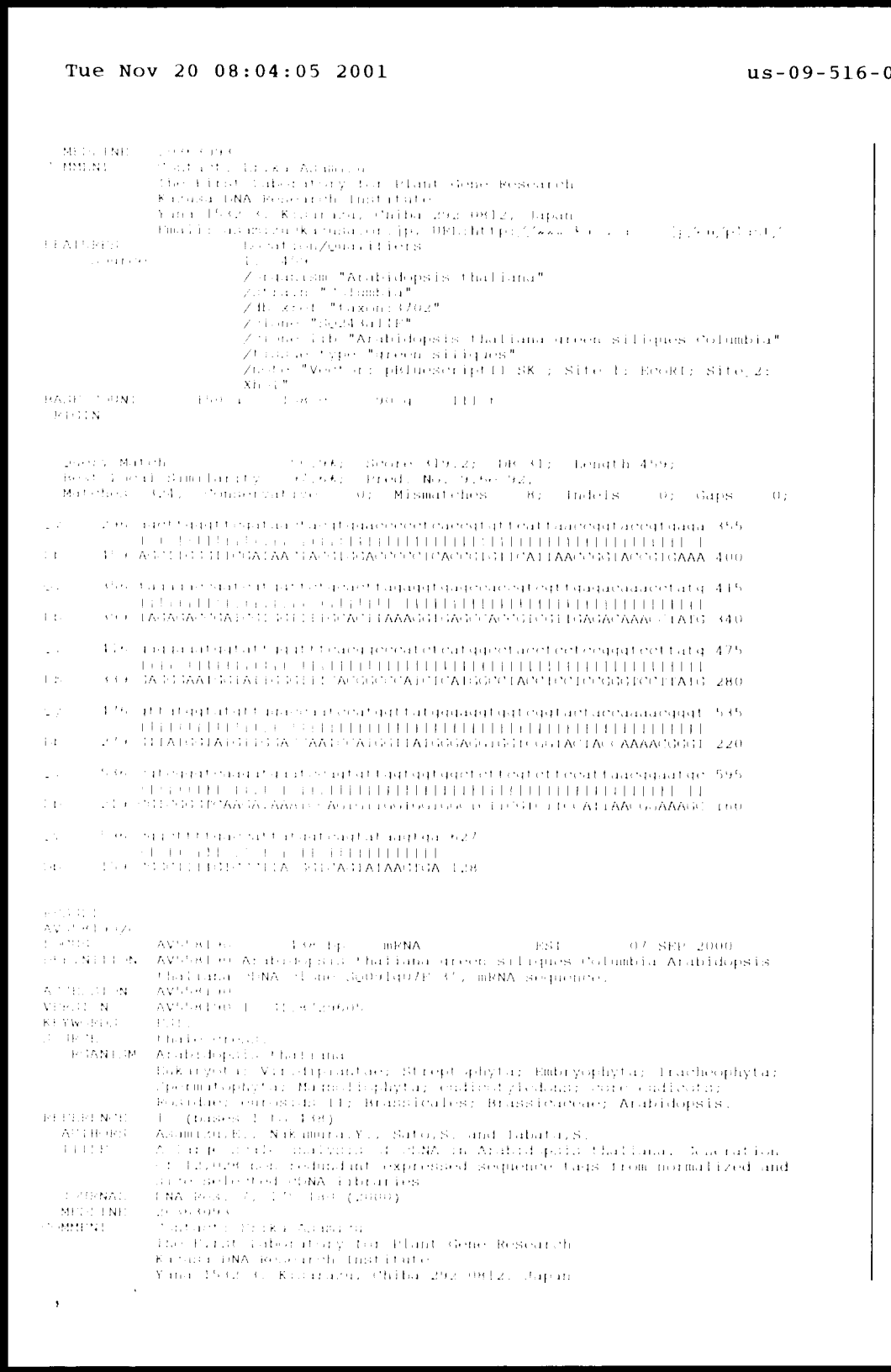

/note= "Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 144 a 82 c 62 g 96 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.8e-56;
Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 419 aaaatgatattgaattcaagaccatctcatgaccaccatcctcaaatcctttatgatt 478
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Db 379 GAAATGGTATTGGGTTCACGGCCATCTCATGGCCTACCTCCTCCGGGTCCTTATGGTT 320

Qy 479 atgatatgttgaaccaatccatcagttatgaaaagtggtcagtactaccaaaacgagtcgt 538
||||||| |||||||||||| ||| ||||||||||||||||||||||||||||||||||||
Db 319 ATGGTATGTTGGACCAATCCATGGTTATGGGAGGTGGTCGGTACTACCAAAACGGGTCGT 260

Qy 539 cgaatcaaaatgaatccaattattgatgtgctcttctcttccattaacgaaatccgaa 598
|||||||-|||||||||||| ||| |||||||||||||||||||||||||||||||||||
Db 259 CGGGTCAAGATGAATCCAGTTGTTGTGGTGGTTCTTCGTCTTCCATTAACCGAATCCCCC 200

Qy 599 ctttgaccattatgatcagtataaatga 627
|||||| |||||||||||, |||'|||
Db 199 CTTTGAACATTATGGTCAGTATAACTGA 171

RESULT 5
BG551755
LOCUS BG551755 497 bp mRNA EST 09-APR-2001
DEFINITION sa41c11.st Gm-c1075 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1075-669 5' similar to TR:O81130 O81130 CCAAT-BOX BINDING FACTOR HAP3 HOMOLOG. [1] ;, mRNA sequence.
ACCESSION BG551755
VERSION BG551755.1 GI:13564585
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE 1 (bases 1 to 497)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,R., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,K., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0930 or (314) 427 3222 FAX:(888) 929 3324 or (314) 427-3424 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com
High-quality sequence stop: 370.
FEATURES Location/Qualifiers
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/clone_lib="Gm-c1075"
/tissue_type "differentiating somatic embryos cultured on MSMSAC"
/lab_host "DH10B"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from differentiating somatic embryos cultured on MSMSAC. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DH10B host cells. Tissue culture and library construction were performed by Francoise Thibaud-Nissen and Ami Khana (Lila Vodkin lab, University of Illinois)."
BASE COUNT 146 a 130 c 141 g 90 t
ORIGIN

Query Match 29.1%; Score 182.4; DB 155; Length 497;
Best Local Similarity 75.0%; Pred. No. 1.1e-47;
Matches 228; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 72 atgtgtggctgtgaggcaagaccaatacatgccaatcgccaaacgtcataaggaatcatgcg 131
||| || | |||||||| | |||||||||||| ||||| || || ||||||||
Db 179 ATGCACGGTGAGGGAGCAAGACAGGTTCATGCCAATCGCTAACGTGATTAGGATCATGCC 238

Qy 132 taaaacttaccgtctcacgccaaaaatctctgacgacgccaaaggaacgattcaagaatg 191
|| | | || | |||| |||||||| |||| || |||||||| || |||| ||
Db 239 CAAGATTCTCCCTCCACACGCAAAAATCTCGGACGATGCAAAAGAAACAATCCAAGAGTC 298

Qy 192 tgtctccgaatacatcagctcgtgacgatgaagccaacaaa attgccaacgtgagca 251
|| || |||||||||||||| | || |||| || |||||||||||| | ||||
Db 299 CGTGTCTGAGTACATCAGCTTCATCACAGGTGAGGCGAACGAGCGTTGCCAGAGGGAGCA 358

Qy 252 acgtaaagaccataactgctgaaagatatcctttgagctatgaagcaagcttgagttcgataa 311
|| |||||||||| || || || | |||||||| |||||||||||||| |||| |
Db 359 GCGGAAGACCATAACCGCAGAGGACGTGCTTTGGGCCATGAGCAAGCTTGGATTCGACGA 418

Qy 312 ctacgtgaaccccctcaccgtgttcattaacgatccatgagataaaagccgatcgtgag 371
|||| | || || | ||| ||| | || |||| |||||||| | ||| || ||
Db 419 CTACATCGAACCGTTGACCATGTACCTTCACCGCTACCGTGAACTTGAGGGTGACCGCAC 478

Qy 372 ttct 375
|||
Db 479 CTCT 482

RESULT 6
AW432980
LOCUS AW432980 551 bp mRNA EST 18-JUL-2000
DEFINITION si23a07.y1 Gm-c1029 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1029-97 5' similar to TR:O81130 O81130 CCAAT-BOX BINDING FACTOR HAP3 HOMOLOG. ;, mRNA sequence.
ACCESSION AW432980
VERSION AW432980.1 GI:6964287
KEYWORDS EST.
SOURCE soybean.
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE 1 (bases 1 to 551)
AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,R., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,K., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE Public Soybean EST Project
JOURNAL Unpublished (1999)
COMMENT Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine

```
            1444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: Genome Systems, Inc. 4633 World
            Parkway Circle St. Louis, Missouri 63134 For further information
            call: (800) 430-0030 or (314) 427 3222 FAX:(888) 919 3324 or (314)
            427 3324 or contact: clones@genomesystems.com or
            info@genomesystems.com web site: www.genomesystems.com
            Insert length: 1267  Std Error: 0.00
            High quality sequence stop: 495.
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                      /tissue_type="very young cotyledons of greenhouse grown
                      plants"
                      /lab_host="DH10B"
                      /note="Vector: pSPORT1; Site 1: Not I; Site 2: Sal I; This
                      cDNA library was constructed from mRNA isolated from very
                      young cotyledons (20 bumps fresh weight) of greenhouse
                      grown plants.  The library was prepared using the Life
                      Technologies pSuperScript cDNA library construction kit.
                      Complementary DNA was synthesized from mRNA using a
                      poly(dT) sequence with a Not I restriction site.  Sal I
                      linker adapters were ligated to the blunt ended cDNA
                      fragments followed by Not I digestion.  The cDNA fragments
                      were directionally cloned into the Not I Sal I restriction
                      site of the pSPORT1 vector.  The ligated cDNA fragments
                      were transformed into E.coli ElectroMax DH10B host cells.
                      This library was constructed by Dr. Paul Keim and Dr.
                      Virginia Cryderman."
BASE COUNT       156 a    137 c    144 g    104 t
ORIGIN


  Query Match             29.1%;  Score 182.4;  DB 116;  Length 551;
  Best Local Similarity   75.0%;  Prob. No. 1.1e-47;
  Matches  228;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy      72 atqtqtqqctcqtqaqcaaqaccaatacatqccaatcqccaaacqtcataaqaatcatqcq 131
           |||   ||   | ||||||||   | ||||||||||| ||||| || || ||||||||
Db     170 AtGCACGGTGAcGGAGCAAGAcAGGTtCATGCCAAtCGCTAACGTGATTAcGAtCAtGCG 229

Qy     132 taaaacttaccqtctcqcqccaaaatctctqacqaqccaaaqaaacqattcaaqaatq 191
           || |   | ||  | |||| |||||||| |||| || |||||||| || ||||| ||
Db     225 CAAGATtCtCCCtCCACACGCAAAAAtCtCGGACGAtGCAAAAGAAACAAtCCAACGAtG 284

Qy     192 tqtctcqqaqtacatcaqcttcqtqaccqatqaaqccaacqaqcqttccaacqtcaqca 251
           || || |||||||||||||| | || |||| || |||||||||||| | ||||
Db     285 cGtGtCtGAGtACAtcAGCttCtCAtCACGGTGAGGCGAACGAGCGTtGCCAGAGCGCA 344
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ACCESSION   AW756413
VERSION     AW756413.1  GI:7685765
KEYWORDS    EST.
SOURCE      soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE   1  (bases 1 to 591)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
            ,A., Bolla,B., Marra,M., Billier,L., Kucaba,T., Martin,J., Beck,C.,
            Wylie,T., Underwood,K., Steptoe,M., Theisinn,B., Allen,M., Bowers
            ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
            ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
            ,R., Waterston,R. and Wilson,R.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: Genome Systems, Inc. 4633 World
            Parkway Circle St. Louis, Missouri 63134 For further information
            call: (800) 430 0030 or (314) 427 3222 FAX:(888) 919 3324 or (314)
            427 3324 or contact: clones@genomesystems.com or
            info@genomesystems.com web site: www.genomesystems.com
            Insert length: 1034  Std Error: 0.00
            High quality sequence stop: 434.
FEATURES              Location/Qualifiers
     source           1..591
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                      /clone_lib="Gm-c1036"
                      /tissue_type="somatic embryos cultured on MSD 20"
                      /lab_host="DH10B"
                      /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; This
                      cDNA library was constructed from mRNA isolated from
                      somatic embryos (age ranging from 2 months to 9 months)
                      cultured on MSD 20. The library was prepared using the
                      Life Technologies pSuperScript cDNA library construction
                      kit. Complementary DNA was synthesized from mRNA using a
                      poly (dT) sequence with a NotI restrictions site. SalI
                      linkers adapters were ligated to the blunt ended cDNA
                      fragments followed by NotI digestion. The cDNA fragments
                      were directionally cloned into the NotI SalI restriction
                      site of the pSPORTI vector. The ligated cDNA fragments
                      were transformed into E.coli ElectroMax DH10B host cells.
                      This library was constructed in the laboratory of Dr. Lila
                      Vodkin by Anu Khanna at the University of Illinois at
                      Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"
BASE COUNT       163 a    157 c    158 g    113 t
ORIGIN


  Query Match             29.1%;  Score 182.4;  DB 120;  Length 591;
  Best Local Similarity   75.0%;  Prob. No. 1.2e-47;
  Matches  228;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy      72 atqtqtqqctcqtqaqcaaqaccaatacatqccaatcqccaaacqtcataaqaatcatqcq 131
           |||   ||   | ||||||||   | ||||||||||| ||||| || || ||||||||
Db     165 ATGCACGGTGACGGAGCAAGACAGGTTCATGCCAATCGCTAACGTGATTACGATCATGCG 224

Qy     132 taaaacttaccqtctcqcqccaaaatctctqacqaqccaaaqaaacqattcaaqaatq 191
           || |   | ||  | |||| |||||||| |||| || |||||||| || ||||| ||
Db     225 CAAGATTCTCCCTCCACACGCAAAAATCTCGGACGATGCAAAAGAAACAATCCAACGATG 284

Qy     192 tqtctcqqaqtacatcaqcttcqtqaccqatqaaqccaacqaqcqttccaacqtcaqca 251
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Db     285 CGTGTCTGAGTACATCAGCTTCTCATCACGGTGAGGCGAACGAGCGTTGCCAGAGCGCA 344
```

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Qy      252 acgtcaaacccataactcctcaaaatatccttcaqqctatqaqccaaqcttqqattcqataa 311
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Db      345 GCGGAAGACCATAACCGCAGAGGACGTGCTTGGGCCATGAGCAAGCTTGGATTCGACGA 404

Qy      312 ctacqtqqacccccctcaccqtqttcattaaccqqtaccqtqaqatataaqaccqatcctaq 371
            |||| | || ||  | ||| ||| | || |||| |||||||| | |||  || ||
Db      405 CTACATCGAACCGTTGACCATGTACCTTCACCGCTACCGTGAACTTGAGGTGACCGCAC 464

Qy      372 ttct 375
            ||||
Db      465 CTCT 468


RESULT   8
BF505304
LOCUS       BF505304       470 bp    mRNA            EST       12-DEC-2000
DEFINITION  sbz52c03.yl Gm-c1055 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
            Gm-c1055-4563 5' similar to TR:Q81130 Q81130 CCAAT BOX BINDING
            FACTOR HAP5 HOMOLOG, [1] :, mRNA sequence
ACCESSION   BF505304
VERSION     BF505304.1  GI:11687628
KEYWORDS    EST.
SOURCE      Soybean.
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE   1  (bases 1 to 470)
  AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Retzel,E., Clifton,S.,
            Waterston,R., Smoller,D., Coryell,V., Khanna,A., Marek,L.,
            Sun,G., Yan,Y., Bowers,Y., Cianzio,S., Scheuring,C., Rineer,J.,
            Slater,S., Hyman,T., Ma,J., Lamb,J., Bhagat,S., Arredondo,J.,
            Wing,R., Soderlund,C., Mahairas,G., Quackenbush,J., Town,C.,
            Walbot,V., Hoffman,E., Cregan,P., Specht,J., Stephenson,P.,
            Collura,K., Shultz,J., Huang,E., Messina,D., Nguyen,H., Wu,G.,
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            Graham,M., Matsye,P., Kim,D., Ehlke,N., Yu,O., Arelli,P.,
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            Nguyen,T., Shannon,J., Clemente,T., Taylor,C., Lohnes,D.,
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            Akkaraju,S., Pan,J., Scheffler,B., Timmerman-Vaughan,G.,
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            Xavier,K., Wang,H., Olhoft,P., Gonzalez,D., Hale,W., Horvath,D.,
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            Bilyeu,K., Sleper,T., Mansur,L., Morey,K., Abe,J., Ishimoto,M.,
            Robertson,D., Welelkes,L., Singer,T., Vodkin,C., Danesh,D.,
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            Vallejos,C., Chen,P., Sebastian,S., Skoneczka,J., Yuan,J.,
            Maroof,S., Buss,G., Lenderts,B., Glover,K., Wesley,R., Poysa,V.,
            Yu,K., Soards,A., Webb,D., Kumar,L., Precetti,C., Woodward,K.,
            Ware,J., Gardner,H., Kicher,T., Gillman,C., Matsumoto,T.,
            Yoshioka,T., Mianoki,S., Tanaka,T., Arai,S., Kawasaki,S.,
            Cianzio,S., Bush,D., Clabotti,P., Porter,R., Spinner,N.,
            Armstrong,J., Gesteland,R., Kadwell,S., Uknes,S., Moskal,W.,
            Granger,C., Hartzell,A., Harada,J., Klein,K., Gregory,B.
  TITLE     Public Soybean EST Project
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: Genome Systems, Inc. 4633 World
            Parkway Circle St. Louis, Missouri 63134 For further information
            call: (800) 430 6030 or (314) 427-2222 FAX:(888) 919-3324 or (314)
            427-3324 or contact: clones@genomesystems.com or
            info@genomesystems.com web site: www.genomesystems.com
            High quality sequence stop: 420.
FEATURES             Location/Qualifiers
     source          1..470
                     /organism="Glycine max"
                     /db_xref="taxon:3847"
                     /clone="GENOME SYSTEMS CLONE ID: Gm-c1055-4563"
                     /clone_lib="Gm-c1055"
                     /tissue_type="Mature seed pods, greenhouse grown"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
                     XhoI; The cDNA library was constructed from mRNA isolated
                     from mature seed pods of greenhouse grown plants prior to
                     senescence for the cultivar KP1. Complementary DNA was
                     synthesized from mRNA using a primer consisting of a
                     poly(dT) sequence with a XhoI restriction site. EcoRI
                     adapters were ligated  to the blunt-ended cDNA fragments
                     followed by XhoI digestion. The cDNA  fragments were
                     directionally cloned into the EcoRI-XhoI restriction site
                     of  the pBluescript vector. The ligated cDNA fragments
                     were transformed into  DH10B host cells (GibcoBRL). This
                     library was constructed in the laboratory of Dr. Randy
                     Shoemaker."
BASE COUNT       138 a    126 c    122 g     84 t
ORIGIN


  Query Match             28.7%;  Score 180.2;  DB 151;  Length 470;
  Best Local Similarity   76.5%;  Pred. No. 5.5e-47;
  Matches  221;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy       72 atgtqtqqctcqtqaqccaaqaccqatacatqccqatcqccaaaccqtcataaqaatcatqcc 131
            |||   ||   | |||||||||   | ||||||||||| |||| || || ||||||||
Db      166 ATGCACGGTGAGGGAGCAAGACAGGTTCATGCCAATCGCCAACGTGATTAGGATCATGCG 225

Qy      132 taaaaccttaccqatctcacqccaaaatctctqacqaccqccaaaqaaaccqattccaqaatq 191
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Db      226 CAAGATTCTCCCTCCACACGCAAAAATCTCGGACCATGCAAAAGAAACAATCCAAGAGTG 285

Qy      192 tqtctccqaqtacatcaqcttcqtqaccqqtqaaqccaacqaqccqttqccaacqtqaqcc 251
            || || ||||||||||||||| | || ||||| || |||||||||||||  | |||||
Db      286 CGTGTCTCAGTACATCAGCTTCATCACAGGTGAGCCGAACGAGCGTTGCCAGAGGGAGCA 345

Qy      252 acgtcaaacccataactcctcaaaatatccttcaqqctatqaqccaaqcttqqattcqataa 311
            || |||||||||| || | || : ||||||| ||||||||||||| |||| | | |
Db      346 GCGGAAGACCATAACCGCAGAGGACGTGCTTGGGCCATGAGCAAGCTTGGATTCGACGA 405

Qy      312 ctacqtqqacccccctcaccqtqttcattaaccqqtaccqtqaqatataaq 360
            |||| | || ||  | ||| ||| | || |||| |||||||  | |||
Db      406 CTACATCGAACCGTTGACCATGTACCTTCACCGCTACCGTGAACTTGAG 454


RESULT   9
AU088581
LOCUS       AU088581       695 bp    mRNA            EST       31-MAR-2000
DEFINITION  AU088581 Rice callus oryza sativa subsp. japonica cDNA clone C52742
            , mRNA sequence.
ACCESSION   AU088581
VERSION     AU088581.1  GI:7378310
KEYWORDS    EST.
SOURCE      Oryza sativa subsp. japonica.
  ORGANISM  Oryza sativa subsp. japonica
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 695)
  AUTHORS   Sasaki,T. and Yamamoto,K.
  TITLE     Rice cDNA from callus (2000)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takuji Sasaki
            National Institute of Agrobiological Resources
            Rice Genome Research Program
            2-1-2 Kannondai,Tsukuba
            Ibaraki,
            Japan 305
            Tel: 0298-38-7441
            Fax: 0298-38-7468
            Email: tsasaki@abr.affrc.go.jp
            PROJECT ='RGP'.
            C52742_12A.
FEATURES             Location/Qualifiers
     source          1..695
                     /organism="Oryza sativa subsp. japonica"
                     /strain="cultivar Nipponbare, sub_species Japonica"
                     /db_xref="taxon:39947"
                     /clone="C52742"
                     /clone_lib="Rice callus"
                     /note="Vector: pBluescript II SK+; Site 1: SalI; Site 2:
                     NotI; cDNA prepared from rice callus mRNAs by using
                     oligo(dT) as a primer and ligating to the SalI NotI site
                     of pBluescript II SK+ phagemid. "
BASE COUNT       124 a    245 c    232 g     88 t      6 others
ORIGIN


  Query Match             26.4%;  Score 165.6;  DB 107;  Length 695;
  Best Local Similarity   73.9%;  Pred. No. 3.1e-42;
  Matches  210;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;
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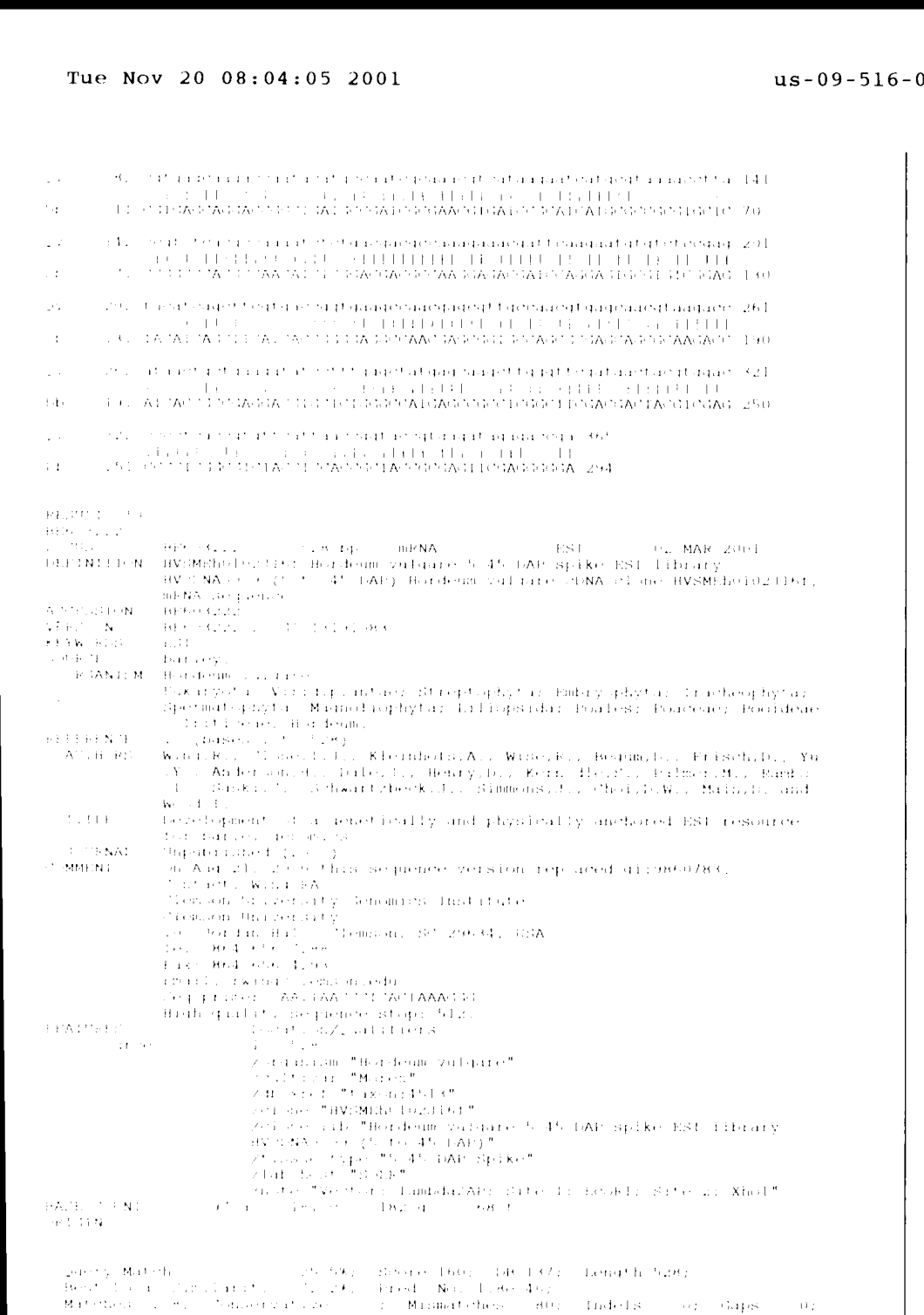

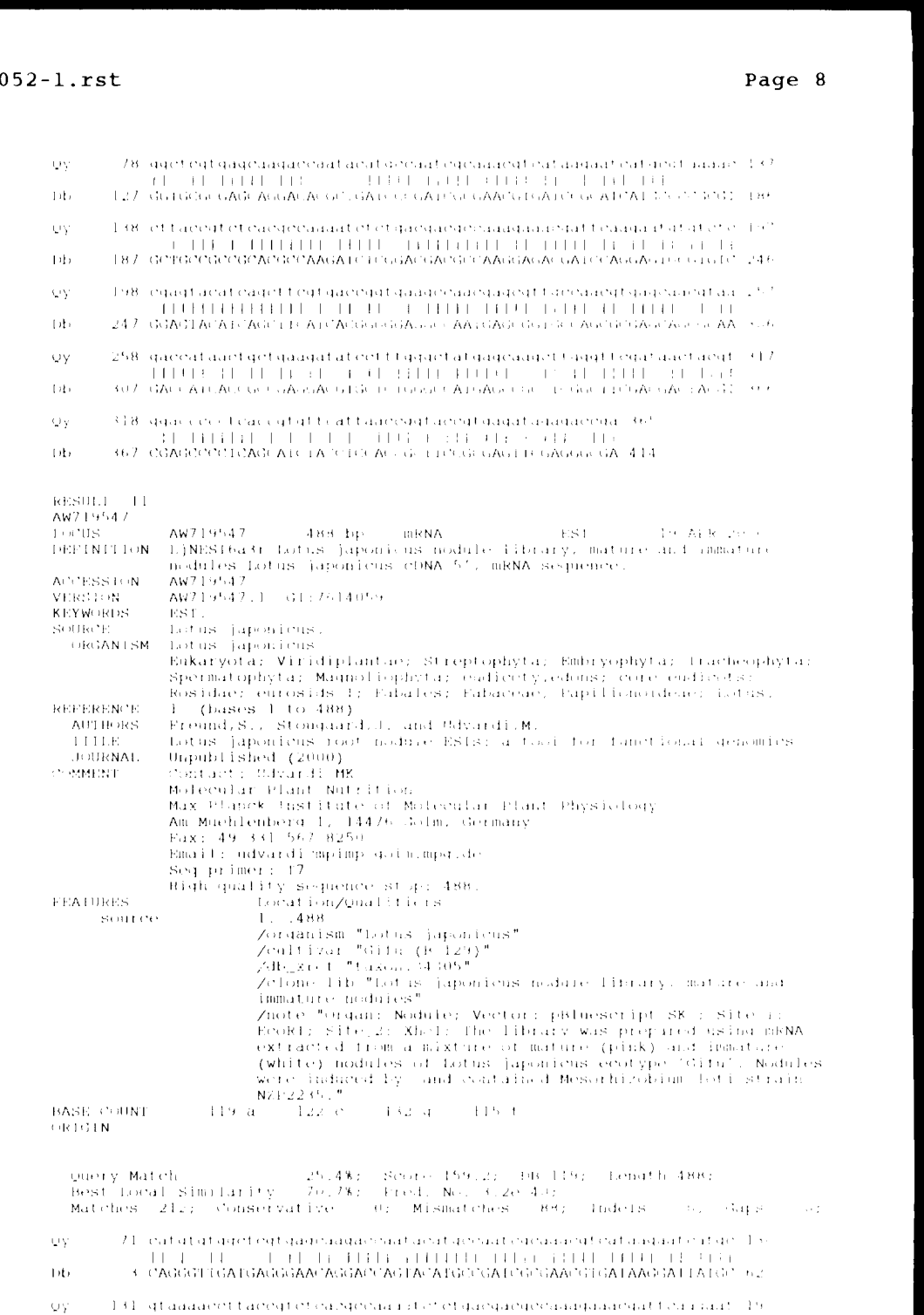

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Db      63 GAAGGAGTCTTCCACGCCAGGCAAAATCTCCGACCAGGCGAAGGAGACGATTCAAGAGT 122

Qy     191 gtgtctcctgaatacatcaactttgtgaccgatgaaacccaacgagcattgccgaccatgaac 250
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Qy     251 aacgtaagaccataactgctgaaagatatcctttgggctatgaagcaagcttgaggttcgata 310
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Db     183 AGAGGAAGACGGTGAGCGCAGAGGACGTGCTTTGGGCGTTTGGGAAGCTTGGCTTCGATG 242

Qy     311 actacgtgaaccccctcaccgtgttcattaacgagtaccgtgaagataagaacccgatcgtg 370
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Db     243 ACTACCTTCTCCCTCTCACCCTTTTCCTTCACCGCTACCGTCACACTGAAGGCGGACTTG 302


RESULT 12
AW720671
LOCUS       AW720671        541 bp    mRNA            EST       19-APR-2000
DEFINITION  LjNS3Barre Lotus japonicus nodule library 5 and 7 week-old Lotus
            japonicus cDNA 5', mRNA sequence.
ACCESSION   AW720671
VERSION     AW720671.1  GI:7615221
KEYWORDS    EST.
SOURCE      Lotus japonicus.
  ORGANISM  Lotus japonicus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotus.
REFERENCE   1  (bases 1 to 541)
  AUTHORS   Sato,S., Erond,S., Trovaskis,B. and Udvardi,M.
  TITLE     Lotus japonicus root nodule ESTs: tools for functional genomics
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Udvardi MK
            Molecular Plant Nutrition
            Max Planck Institute of Molecular Plant Physiology
            Am Muehlenberg 1, 14476 Golm, Germany
            Fax: 49 331 567 8250
            Email: udvardi@mpimp-golm.mpg.de
            Seq primer: P7
            High quality sequence stop: 531.
FEATURES             Location/Qualifiers
     source          1..541
                     /organism="Lotus japonicus"
                     /cultivar="Gifu (B-129)"
                     /db_xref="taxon:34305"
                     /clone_lib="Lotus japonicus nodule library 5 and 7
                     week-old"
                     /dev_stage="5 and 7 week old plants"
                     /note="Organ: Nodule; Vector: pSPORT1; Site_1: Sal1;
                     Site_2: Not1; The library was prepared using mRNA
                     extracted from nodules of 5 and 7 week-old Lotus plants.
                     Nodules were induced by, and contained Mesorhizobium
                     strain R7A."
BASE COUNT       127 a    129 c    143 g    132 t
ORIGIN

  Query Match             25.4%;  Score 159.2;  DB 119;  Length 541;
  Best Local Similarity   70.7%;  Pred. No. 3.3e-40;
  Matches  212;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy      71 catgtatgtgactcgtgaagcaagccaatacatgccaatccgcaaaacgtcgtcaaaaatcatc 130
           || | ||   | || || |||| |||||||| |||| |||| |||| || ||||
Db       3 CAAGGTTGATCAGCGAACAGCAGCAGCACATGCCGATCGCGAACGTGATAAGGATTATGC 62

Qy     131 gtaaaacgttacgtctcacgccaaaatctctgaacgacgccaaagaaaacgattcaaaaat 190
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Db      63 GAAGGAGTCTTCCACGCCAGGCAAAATCTCCGACCAGGCGAAGGAGACGATTCAAGAGT 122

Qy     191 gtgtctcctgaatacatcaactttgtgaccgatgaaacccaacgagcattgccgaccatgaac 250
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Db     123 GCGTGTCGGAGTTCATCAGCTTCGTTACTTCCGAAGCTAATGAGCGGTGCCAGAAGGAGC 182

Qy     251 aacgtaagaccataactgctgaaagatatcctttgggctatgaagcaagcttgaggttcgata 310
           | | ||||  | |  || || ||  | ||||||||  |  | |||||||| || |||
Db     183 AGAGGAAGACGGTGAGCGCAGAGGACGTGCTTTGGGCGTTTGGGAAGCTTGGCTTCGATG 242

Qy     311 actacgtgaaccccctcaccgtgttcattaacgagtaccgtgaagataagaacccgatcgtg 370
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Db     243 ACTACCTTCTCCCTCTCACCCTTTTCCTTCACCGCTACCGTCACACTGAAGGCGGACTTG 302


RESULT 13
AL509098
LOCUS       AL509098        441 bp    mRNA            EST       04-JAN-2001
DEFINITION  AL509098 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
            Hordeum vulgare cDNA clone HY10L07V 5', mRNA sequence.
ACCESSION   AL509098
VERSION     AL509098.1  GI:12035601
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 441)
  AUTHORS   Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
  TITLE     EST sequencing and analysis in barley
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Michalek W
            Institute for Plant Genetics and Crop Plant Research
            Corrensstr.3, D-06466 Gatersleben, Germany
            email: michalek@ipk-gatersleben.de, tel: 49-39482-5284, fax: ipk gatersleben.de
            Seq primer: T3 primer for 5'end.
FEATURES             Location/Qualifiers
     source          1..441
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                     /cultivar="Barke"
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                     /clone="HY10L07V"
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                     (3.-15.DAP)"
                     /tissue_type="developing caryopsis (3.-15.DAP)"
                     /lab_host="XL0LR"
                     /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2:
                     XhoI; mRNA was made from developing caryopsis (3.-15.DAP)
                     of spring barley variety 'Barke', a high quality malting
                     variety. Cloning sites: EcoRI (5' end of cDNA) and XhoI
                     (3'-end of cDNA). NOTE: Due to a cloning artefact caused
                     by the kit, in most cases the EcoRI site is NOT present,
                     as well as the EcoRI adapter. Average insert size is 1 kb
                     Sequence trimming: Vector sequences and sequence ends were
                     trimmed from the 5'-and 3'-end until a 50 bp window
                     contains less than two ambiquities. The maximum length was
                     set to 700 bp"
BASE COUNT        84 a    150 c    141 g     62 t      4 others
ORIGIN

  Query Match             25.2%;  Score 158;  DB 105;  Length 441;
  Best Local Similarity   68.5%;  Pred. No. 7.7e-40;
  Matches  215;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy      76 qtqqctcqtqaqcaaqaccaatacatqccaatccqcaaaacgtcgtcaaaaatcatcgcgtaaa 135
           ||||  || |||||  ||||        ||||| ||||| ||||| ||  | |||||||
Db     102 GTGGTGCGGGAGCAGGACCGGCTGATGCAGATCGCGAACGTGATCCGNATCATGCGCCGT 161

Qy     136 acgttacgctctcacgccaaaatctctgaacgacgccaaagaaaacgattcaaaaatgtgtc 195
           | | ||  | |||||||| ||||| ||||||||||| ||  |||| || || || ||
Db     162 GCGCTCCCTGCCCACGCCAAGATCTCCGACGACGCCAANGAGGCGATCCAGGAGTGCGTG 221

Qy     196 tccgaqtacatcaqcttcqtqacqqqtqaaqccaacqaqcattgccaacgtgacgaccgt 255
           || |||| |||||||||||| ||||| || ||| || |||| ||||||    |||| ||
Db     222 TCGGAGTTCATCAGCTTCGTCACGGGCGAGGCCAACTACGCGTGCCACATCGACGCCAACGC 281

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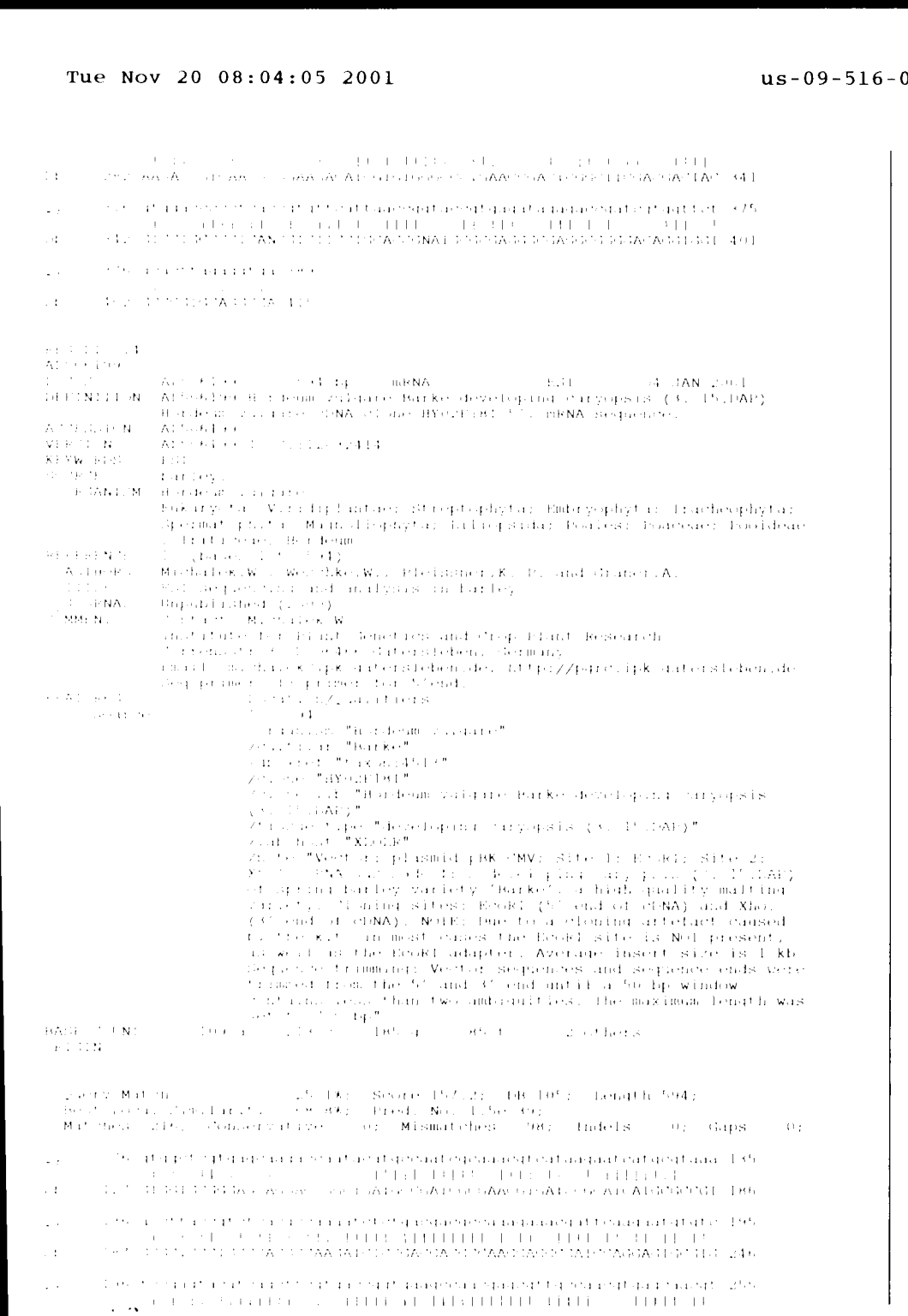

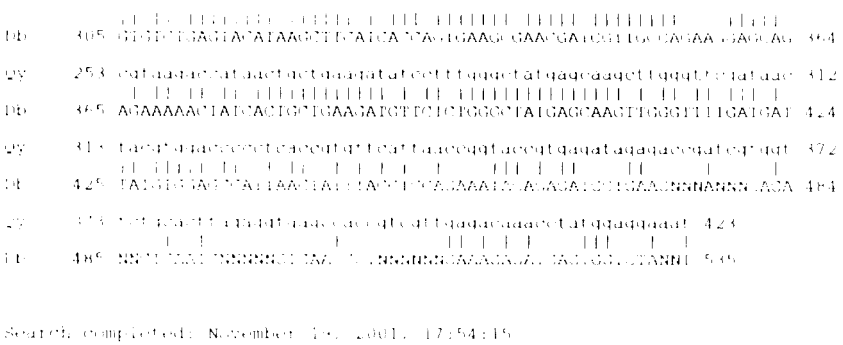

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